

SEQUENCE LISTING

<110> WALLACH, David
BOLDIN, Mark
VARFOLOMEEV, Eugene
METT, Igor

<120> MODULATORS OF THE FUNCTION OF FAS/APO1 RECEPTORS

<130> WALLACH=16B

<150> 08/860,082

<151> 1997-08-19

<150> PCT/US95/16542

<151> 1995-12-14

<150> IL 112022

<151> 1994-12-15

<150> IL 112692

<151> 1995-02-19

<160> 2

<170> PatentIn version 3.0

<210> 1

<211> 1701

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(768)

<400> 1

gtg aat cag gca ccg gag tgc agg ttc ggg ggt gga atc ctt ggg ccg	48
Val Asn Gln Ala Pro Glu Cys Arg Phe Gly Gly Gly Ile Leu Gly Pro	
1 5 10 15	
ctg ggc aag cgg cga gac ctg gcc agg gcc agc gag ccg agg aca gag	96
Leu Gly Lys Arg Arg Asp Leu Ala Arg Ala Ser Glu Pro Arg Thr Glu	
20 25 30	
ggc gcg cgg agg gcc ggg ccg cag ccc cgg ccg ctt gca gac ccc gcc	144
Gly Ala Arg Arg Ala Gly Pro Gln Pro Arg Pro Leu Ala Asp Pro Ala	
35 40 45	
atg gac ccg ttc ctg gtg ctg ctg cac tcg gtg tcg tcc agc ctg tcg	192
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser	
50 55 60	
agc agc gag ctg acc gag ctc aag ttc cta tgc ctc ggg cgc gtg gtc	240
Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Val	
65 70 75 80	
aag cgc aag ctg gag cgc gtg cag agc ggc cta gac ctc ttc tcc atg	288
Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met	
85 90 95	
ctg ctg gag cag aac gac ctg gag ccc ggg cac acc gag ctc ctg cgc	336
Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg	

100	105	110	
gag ctg ctc gcc tcc ctg cgg cgc cac gac ctg ctg cgg cgc gtc gac			384
Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp			
115	120	125	
gac ttc gag gcg ggg gcg gcc ggg gcc gcg cct ggg gaa gaa gac			432
Asp Phe Glu Ala Gly Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp			
130	135	140	
ctg tgt gca gca ttt aac gtc ata tgt gat aat gtg ggg aaa gat tgg			480
Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp			
145	150	155	160
aga agg ctg gct cgt cag ctc aaa gtc tca gac acc aag atc gac agc			528
Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser			
165	170	175	
atc gag gac aga tac ccc cgc aac ctg aca gag cgt gtg cgg gag tca			576
Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser			
180	185	190	
ctg aga atc tgg aag aac aca gag aag gag aac gca aca gtg gcc cac			624
Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His			
195	200	205	
ctg gtg ggg gct ctc agg tcc tgc cag atg aac ctg gtg gct gac ctg			672
Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu			
210	215	220	
gta caa gag gtt cag cag gcc cgt gac ctc cag aac agg agt ggg gcc			720
Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala			
225	230	235	240
atg tcc ccg atg tca tgg aac tca gac gca tct acc tcc gaa gcg tcc			768
Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser			
245	250	255	
tgatggggccg ctgctttgcg ctggtggacc acagggcatct acacagcctg gactttgggt			828
ctctccagga aggtagccca gcaactgtgaa gacccagcag gaagccaggc tgagttagcc			888
acagaccacc tgcttctgaa ctcaagctgc gtttattaat gcctctcccg caccaggccg			948
ggcttggggcc ctgcacagat atttccattt ctctctcact atgacactga gcaagatctt			1008
gtctccacta aatgagctcc tgcgggagta gttggaaagt tggaaccgtg tccagcacag			1068
aaggaatctg tgcagatgag cagtcacact gttactccac agcggaggag accagctcag			1128
aggcccagga atcggagcga agcagagagg tggagaactg ggatttgaac ccccgccatc			1188
cttcaccaga gcccattgtc aaccactgtg gcgttctgct gcccctgcag ttggcagaaa			1248
ggatgttttt gtcccatttc cttggaggcc accgggacag acctggacac tagggtcagg			1308
cggggtgctg tgggtggggag aggcattggt ggggtggggg tggggagacc tggttggccg			1368
tgggtccagct cttggccct gtgtgagttg agtctctct ctgagactgc taagtagggg			1428
cagtgatggt tgccaggacg aattgagata atatctgtga ggtgctgatg agtgattgac			1488
acacagcact ctctaaatct tccttgtgag gattatgggt cctgcaattc tacagtttct			1548

tactgttttg tatcaaaatc actatctttc tgataacaga attgccaagg cagcgggatc 1608
 tcgtatcttt aaaaagcagt cctcttattc ctaaggtaat cctattaaaa cacagcttta 1668
 caacttccat attacaaaaa aaaaaaaaaa aaa 1701

<210> 2
 <211> 256
 <212> PRT
 <213> Homo sapiens

<400> 2

Val Asn Gln Ala Pro Glu Cys Arg Phe Gly Gly Gly Ile Leu Gly Pro
 1 5 10 15

Leu Gly Lys Arg Arg Asp Leu Ala Arg Ala Ser Glu Pro Arg Thr Glu
 20 25 30

Gly Ala Arg Arg Ala Gly Pro Gln Pro Arg Pro Leu Ala Asp Pro Ala
 35 40 45

Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
 50 55 60

Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Val
 65 70 75 80

Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
 85 90 95

Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
 100 105 110

Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
 115 120 125

Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
 130 135 140

Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
 145 150 155 160

Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
 165 170 175

Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
 180 185 190

Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
195 200 205

Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
210 215 220

Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
225 230 235 240

Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
245 250 255

09033814-082201